

# RECEIVED

JUN 21 2001

Page 1 of 7

1647  
#12  
NB  
06/22/01

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/397,846B

TECH CENTER 1600/2900 /600  
DATE: 05/21/2001  
TIME: 11:35:48

Input Set : A:\98-54.SEQ.txt  
Output Set: N:\CRF3\05212001\I397846B.raw

# ENTERED

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3 <110> APPLICANT: Presnell, Scott R.
4   Taft, David W.
5   Foley, Kevin P.
8 <120> TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
10 <130> FILE REFERENCE: 98-54
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/397,846B
C--> 12 <141> CURRENT FILING DATE: 2001-05-21
12 <150> PRIOR APPLICATION NUMBER: 60/100,706
13 <151> PRIOR FILING DATE: 1998-09-17
15 <160> NUMBER OF SEQ ID NOS: 22
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1819
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (71)...(676)
28 <400> SEQUENCE: 1
29   cgggcgcggg ggcgcaggcgg gctcctccgg cgcgtgcgga cgcgtgagcgt ggcctgtccc      60
30   tcaggtctgg atg ctg gta gcc ggc ttc ctg ctg gcg ctg ccg ccg agc      109
31       Met Leu Val Ala Gly Phe Leu Leu Ala Leu Pro Pro Ser
32       1           5           10
34   tgg gcc gcg gcc gcc ccg agg gcg gcc agg cgc ccc gcg cgg ccg cgg      157
35   Trp Ala Ala Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg
36       15           20           25
38   ggc tgc gcg gac cgg ccg gag gag cta ctg gag cag ctg tac ggg cgc      205
39   Gly Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg
40   30           35           40           45
42   ctg gcg gcc gcc gtg ctc agt gcc ttc cac cac acg ctg cag ctg ggg      253
43   Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly
44       50           55           60
46   ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca ggg ggc agg ccc      301
47   Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro
48       65           70           75
50   gcc gac cgc cgc ttc cgg ccg ccc acc aac ctg cgc agc gtg tcg ccc      349
51   Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro
52       80           85           90
54   tgg gcc tac aga atc tcc tac gac ccg gcg agg tac ccc agg tac ctg      397
55   Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu
56       95           100          105
58   cct gaa gcc tac tgc ctg tgc cgg gcc tgc ctg acc ggg ctg ttc ggc      445
59   Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly
60   110          115          120          125
62   gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac atg ccc acc gtc      493
63   Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val
64       130          135          140

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66  gtc ctg cgc cgc acc ccc gcc tgc gcc gcc ggc cgt tcc gtc tac acc      541
67  Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr
68              145              150              155
70  gag gcc tac gtc acc atc ccc gtg gcc tgc acc tgc gtc ccc gag ccg      589
71  Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro
72              160              165              170
74  gag aag gac gca gac agc atc aac tcc agc atc gac aaa cag gcc gcc      637
75  Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala
76              175              180              185
78  aag ctc ctg ctg gcc ccc aac gac gcg ccc gct gcc ccc tgaggccggt      686
79  Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
80  190              195              200
82  cctgccccgg gaggtctccc cggccccgat cccgaggcgc ccaagctgga gccgcctgga      746
83  gggctcggtc ggcgacctct gaagagagtg caccgagcaa accaagtgcc ggagcaccag      806
84  cgccgccttt ccatggagac tcgtaagcag cttcatctga cacgggaatc cctggcttgc      866
85  ttttagctac aagcaagcag cgtggctgga agctgatggg aaacgacccg gcacgggcat      926
86  cctgtgtgcg gcccgcatgg agggtttgga aaagtgcacg gaggtccctc gaggagcctc      986
87  tcagatcggc tgctgcgggt gcaggcgctg actcacgcgt ggggtgcttgc caaagagata      1046
88  gggacgcata tgctttttaa agcaatctaa aaataataat aagtatagcg actatatacc      1106
89  tacttttaaa atcaactgtt ttgaatagag gcagagctat tttatattat caaatgagag      1166
90  ctactctggt acatttctta acatataaac atcgtttttt acttcttctg gtagaatttt      1226
91  ttaaagcata attggaatcc ttggataaat tttgtagctg gtacactctg gcctgggtct      1286
92  ctgaattcag cctgtcaccc atggctgact gatgaaatgg acacgtctca tctgaccac      1346
93  tcttccttcc actgaaggtc ttcacgggcc tccaggtgga ccaaagggat gcacaggcgg      1406
94  ctcgcatgcc ccagggccag ctaagagttc caaagatctc agatttggtt ttagtcatga      1466
95  atacataaac agtctcaaac tcgcacaatt ttttccccct tttgaaagcc actggggcca      1526
96  atttgtggtt aagaggtggt gagataagaa gtggaacgtg acatctttgc cagttgtcag      1586
97  aagaatccaa gcaggtattg gcttagttgt aagggtttta ggatcaggcc gaatatgagg      1646
98  acaaagtggg ccacgttagc atctgcagag atcaatctgg aggttctgtt ttctgcattc      1706
99  tgccacgaga gctaggtcct tgatcttttc tttagattga aagtctgtct ctgaacacaa      1766
100 ttatttgtaa aagttagaag ttctttttta aatcattaaa agaggcttgc tga      1819
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 202
104 <212> TYPE: PRT
105 <213> ORGANISM: Homo sapiens
107 <400> SEQUENCE: 2
108  Met Leu Val Ala Gly Phe Leu Leu Ala Leu Pro Pro Ser Trp Ala Ala
109    1             5             10             15
110  Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys Ala
111          20             25             30
112  Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala
113        35             40             45
114  Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu
115        50             55             60
116  Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp Arg
117        65             70             75             80
118  Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr
119          85             90             95
120  Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu Ala

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121          100          105          110
122 Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu Asp
123          115          120          125
124 Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu Arg
125          130          135          140
126 Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala Tyr
127 145          150          155          160
128 Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys Asp
129          165          170          175
130 Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu Leu
131          180          185          190
132 Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
133          195          200
135 <210> SEQ ID NO: 3
136 <211> LENGTH: 187
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 3
141 Ala Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys
142 1          5          10          15
143 Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala
144          20          25          30
145 Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg
146          35          40          45
147 Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp
148          50          55          60
149 Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala
150 65          70          75          80
151 Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu
152          85          90          95
153 Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu
154          100          105          110
155 Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu
156          115          120          125
157 Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala
158          130          135          140
159 Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys
160 145          150          155          160
161 Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu
162          165          170          175
163 Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
164          180          185
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 186
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <400> SEQUENCE: 4
172 Gly Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys Ala
173 1          5          10          15

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174 Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala
175           20           25           30
176 Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu
177           35           40           45
178 Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp Arg
179           50           55           60
180 Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr
181           65           70           75           80
182 Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu Ala
183           85           90           95
184 Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu Asp
185           100          105          110
186 Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu Arg
187           115          120          125
188 Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala Tyr
189           130          135          140
190 Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys Asp
191           145          150          155          160
192 Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu Leu
193           165          170          175
194 Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
195           180          185
197 <210> SEQ ID NO: 5
198 <211> LENGTH: 185
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 5
203 Ala Pro Arg Ala Gly Arg Arg Pro Ala Arg Pro Arg Gly Cys Ala Asp
204   1           5           10           15
205 Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala Gly
206           20           25           30
207 Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu Gln
208           35           40           45
209 Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro Ala Asp Arg Arg
210           50           55           60
211 Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr Arg
212           65           70           75           80
213 Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Pro Glu Ala Tyr
214           85           90           95
215 Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly Glu Glu Asp Val
216           100          105          110
217 Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val Val Leu Arg Arg
218           115          120          125
219 Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr Glu Ala Tyr Val
220           130          135          140
221 Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro Glu Lys Asp Ala
222           145          150          155          160
223 Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala Lys Leu Leu Leu
224           165          170          175

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225 Gly Pro Asn Asp Ala Pro Ala Gly Pro
226             180             185
228 <210> SEQ ID NO: 6
229 <211> LENGTH: 23
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 6
234 ccgggtcgta ggagattctg tag                23
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 22
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 7
242 gcgtgctcag tgccttcac ca                22
244 <210> SEQ ID NO: 8
245 <211> LENGTH: 1221
246 <212> TYPE: DNA
247 <213> ORGANISM: Mus musculus
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (79)...(693)
253 <400> SEQUENCE: 8
254 ggggtgcgcc cttatttact tcgcagaaga gccttcagcc cccctcctaa caagtctgga        60
255 aagcatcacg gcgacgcg atg ttg ggg aca ctg gtc tgg atg ctc gcg gtc        111
256             Met Leu Gly Thr Leu Val Trp Met Leu Ala Val
257             1             5             10
259 ggc ttc ctg ctg gca ctg gcg ccg ggc cgc gcg ggc gcg ctg agg        159
260 Gly Phe Leu Leu Ala Leu Ala Pro Gly Arg Ala Ala Gly Ala Leu Arg
261             15             20             25
263 acc ggg agg cgc ccg gcg ccg ccg gac tgc gcg gac cgg ccg gag        207
264 Thr Gly Arg Arg Pro Ala Arg Pro Arg Asp Cys Ala Asp Arg Pro Glu
265             30             35             40
267 gag ctc ctg gag cag ctg tac ggg ccg ctg gcg gcc ggc gtg ctc agc        255
268 Glu Leu Leu Glu Gln Leu Tyr Gly Arg Leu Ala Ala Gly Val Leu Ser
269             45             50             55
271 gcc ttc cac cac acg ctg cag ctc ggg ccg cgc gag cag gcg cgc aat        303
272 Ala Phe His His Thr Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn
273             60             65             70             75
275 gcc agc tgc ccg gcc ggg ggc agg gcc gcc gac cgc cgc ttc cgg cca        351
276 Ala Ser Cys Pro Ala Gly Gly Arg Ala Ala Asp Arg Arg Phe Arg Pro
277             80             85             90
279 ccc acc aac ctg cgc agc gtg tcg ccc tgg gcg tac agg att tcc tac        399
280 Pro Thr Asn Leu Arg Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr
281             95             100             105
283 gac cct gct cgc ttt ccg agg tac ctg ccc gaa gcc tac tgc ctg tgc        447
284 Asp Pro Ala Arg Phe Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys
285             110             115             120
287 cga ggc tgc ctg acc ggg ctc tac ggg gag gag gac ttc cgc ttt cgc        495
288 Arg Gly Cys Leu Thr Gly Leu Tyr Gly Glu Glu Asp Phe Arg Phe Arg

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VERIFICATION SUMMARY                      DATE: 05/21/2001  
PATENT APPLICATION:    US/09/397,846B        TIME: 11:35:49

Input Set : A:\98-54.SEQ.txt  
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date